degenerations; and wherein MOP-C consists of a forward primer which is a nucleotide sequence with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO. 3 with 3072 degenerations, and a reverse primer with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO. 48192 with degenerations; and wherein each of the heads defines a nucleotide sequence comprising an interface for a restriction enzyme and a clamp sequence at a 5' end of the interface and which has a length not exceeding one half of a length of a complete nucleotide sequence of one of the forward or the reverse primer.

11. The primer mixture of claim 10, wherein the head has the sequence GAAGGATCC.

12. The MOP primer mixture of claim 10, for use in detecting and identifying one of, retrovirus or retroviral nucleic acid.

13. A method for specific detection and identification of a retrovirus or retroviral nucleic acid in a specimen comprising the steps of:

- isolating at least one, DNA or RNA from the specimen;
- producing respective amplificates of the DNA or RNA by subjecting said at least one isolated DNA to PCR or isolated RNA to RT-PCR by using a primer mixture of forward and reverse primers;
- purging the amplificates;

- detecting the presence of a retroviral nucleotide sequence of a retrovirus-specific reverse-transcriptase gene or a section thereof by subjecting the amplificates to reverse dot blot hybridization (RDBH) using immobilized RDBH probes, wherein each said probes includes at least one of synthetic oligonucleotide sequences corresponding to the retroviral nucleotide sequence of the retrovirus specific reverse transcriptase gene or a section thereof, and which do not overlap with nucleotide sequences of the forward and reverse primer of the primer mixture.

14. The method of claim 13, wherein the primer mixture comprises at least one of MOP-ABD or MOP-C and wherein MOP-ABD consists of a forward primer with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO. 1 with 3456 degenerations, and a reverse primer with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO.2 with 27648 degenerations; and wherein MOP-C, consists of a forward primer which is a nucleotide sequence with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO. 3 with 3072 degenerations, and a reverse primer with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO. 4 with 8192 degenerations; and wherein each of the heads defines a nucleotide sequence comprising an interface for a restriction enzyme and a clamp sequence at a 5' end of the interface and which has a length not

exceeding one half of a length of a complete nucleotide sequence of one of the forward or the reverse primer.

15. The method of claim 13, wherein each of the RDBH probes correspond to a region of the retroviral nucleic acid of the reverse transcriptase gene between one of, highly conserved motifs V L P Q G and Y M/V D D I/V/L L, or a section of this region.

16. The method of claim 15, wherein each of the immobilized RDBH probes used is a mixture of equimolar quantities of both partners of a pair of synthetic oligonucleotides together corresponding to section from the nucleic acid region of the reverse transcriptase gene between the highly conserved motifs V L P Q G and Y M/V D D I/V/L L .

17. The method of claim 16, wherein the section is 90 base pair long.

18. The method of claim 16, wherein both partners of the pair of synthetic oligonucleotides are approximately the same size or the same length.

19. The method of claim 18, wherein the synthetic oligonucleotides are approximately 45 base pairs long.

20. The method of claim of claim 13, wherein the reverse dot blot hybridization probe used is at least one synthetic oligonucleotide whose nucleotide sequence corresponds with the nucleic acid region of a retrovirus-specific reverse transcriptase gene between one of, highly conserved motifs V L P Q G and Y M/V D D I/V/L L, or with a section of this nucleic acid region.

21. The method of claim 13, wherein equimolar quantities of two synthetic oligonucleotides which together, positioned one after the other, correspond to a section from the nucleic acid region of the reverse transcriptase gene between the highly conserved motifs V L P Q G and Y M/V D D I/V/L L are used as reverse dot blot hybridization probe(s) in a method according to one of claims 3 to 6.

22. The method of claim 21, wherein the section is 90 base pairs long.

23. A diagnostic kit for the specific detection and identification of retroviral nucleic acids and/or retroviruses in an arbitrary specimen comprising:

- at least one of MOP-ABD or MOP-C and wherein MOP-ABD consists of a forward primer with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO. 1 with 3456 degenerations, and a reverse primer with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO.2 with 27648 degenerations; and wherein MOP-C, consists of a forward primer

which is a nucleotide sequence with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO. 3 with 3072 degenerations, and a reverse primer with a head at its 5' end and a nucleotide sequence in accordance with SEQ. ID NO. 4 with 8192 degenerations; and wherein each of the heads defines a nucleotide sequence comprising an interface for a restriction enzyme and a clamp sequence at a 5' end of the interface and which has a length not exceeding one half of a length of a complete nucleotide sequence of one of the forward or the reverse primer; and

- at least one reverse dot blot hybridization probe.

24. The diagnostic kit of claim 23, wherein the reverse dot blot hybridization probe includes at least one synthetic oligonucleotide sequence which corresponds with one of a nucleic acid region of a retrovirus specific reverse transcriptase gene between highly conserved motifs V L P Q G and Y M/V D D I/V/LL or with a section thereof.

25. The diagnostic kit of claim 24, wherein the reverse dot blot hybridization probe includes at least two synthetic oligonucleotides in equimolar quantities positioned one after another and corresponding to a section of about 90 base pairs from a nucleic acid region of a reverse transcriptase gene between highly conserved motifs V L P Q G and Y M/V D D I/V/L L.